Laurent Briollais, Ph.D

ACADEMIC DEGREES

1990	National School of Statistics (ENSAE)	B.Sc.	Statistics/Economy
1994	University of Paris XI	M.Sc.	Biostatistics/Statistical Genetics
1998	University of Paris XI	Ph.D.	Biostatistics/Statistical Genetics

EMPLOYMENT

2016-	Assistant Professor (status-only) - Department of Statistical Sciences, University of Toronto, Toronto, Canada
2013-	Associate Professor (status-only) Dalla Lana School of Public Health Sciences (Biostatistics)
2000-2012	Assistant Professor (status-only) Dalla Lana School of Public Health Sciences (Biostatistics)
2007-present	Senior Scientist in Statistical Genetics/Biostatistics, Lunenfeld Tanenbaum Research Institute of Mount Sinai Hospital
2000-2006	Scientist in Statistical Genetics/ Biostatistics, Lunenfeld Tanenbaum Research Institute of Mount Sinai Hospital
1998-2000	Biostatistician, Hospital Clarac, Martinique, France
1993-1998	Research Assistant in Biostatistics, Hospital Saint Louis, Paris, France
1992-1992	Research Assistant, Research Institute for Exploitation of Sea, Martinique, France
1990-1991	Statistician, National Institute of Statistics, Martinique, France

PROFESSIONAL AFFILIATIONS

- Statistical Society of Canada (SSC)
- International Genetic Epidemiological Society (IGES)
- American Association of Human Genetics (ASHG)
- French Statistical Association (SFdS)
- Member of the Breast and Colon Family Cancer Registries (BCFR & CCFR)
- Member of PRACTICAL consortium **(**Prostate Cancer Association group to Investigate Cancer Associated Alterations in the Genome**)**

COMMITTEE MEMBERSHIPS

- CANSSI (Canadian Statistical Science Institute) Health Science Collaborating Centre for Statistical Omics steering committee
- STAGE (Strategic Training for Advanced Genetic Epidemiology) steering committee
- University of Toronto's Division of Biostatistics Curriculum committee
- University of Toronto's Division of Biostatistics MSc and PhD Admission committees
- University of Toronto's Division of Biostatistics PhD Activity Progress committee
- Family integrated care: data safety monitoring committee (Mount Sinai Hospital)
- Analytic Committee of the EArly Genetics and Lifecourse Epidemiology (EAGLE) consortium
- Publication committee of the International Genetic Epidemiological Society (IGES) in 2009
- Biostatistical mentor in Statistical Genetics, CIHR Strategic Training for Advanced Genetic Epidemiology (STAGE)
- Genetic Epidemiology group of the Western Australian Pregnancy Cohort (RAINE)

JOURNAL REVIEW ACTIVITIES

- Review editor in Frontiers in Statistical Genetics and Methodology since 2011
- Regular reviewer for Statistics in Medicine, Biometrics, PLoS One, American Journal of Human Genetics

- Also reviewed for Annals of Applied Statistics, Genetic Epidemiology, Biostatistics, Bioinformatics, American Journal of Epidemiology, International Journal of Cancer, etc.

GRANT REVIEW ACTIVITIES

- CIHR genetic panel full member since March 2013
- CIHR STAGE fellowship application reviewer for 2014 round
- NSERC discovery grant reviewer (multiple applications since 2012)
- Medical Research Council (MRC) career award reviewer (Sept. 2014)
- MITACS Elevate postdoctoral fellowship application reviewer (2010 round)
- CBCF PhD and postdoctoral fellowship applications (Feb. 2008)

CURRENTLY FUNDED GRANTS

As PI:

2019-2023 CIHR project grant. Extending risk prediction models for hereditary breast ovarian cancer.
Investigators: **Briollais L (PI)**, Choi YH, Andrulis I, Knight J.
Requested: $630,667

2019-2020 McLaughlin Centre Accelerating grant in Genomic Medicine. Team grant.
A unified polygenic risk score analytics platform for risk prediction, causal inference and discovery.
Gagnon F (NPI), Sun L (NPI), **Briollais (PI)**, Bull (PI), Strug L, Wang L, Goncalves V, Paterson A, Brooks J.
$375,000.

2019-2021 Statistical Methods for the Analysis of Genetic Data with Survival Outcomes.
Lakhal-Chaieb L, **Briollais L**, Cook R.
$180,0000
CANSSI Collaborative Research Team Project.

2015-2020 Development of Bayesian Graphical Models for Next-Generation Genetic Studies
Investigators: **Briollais L** (PI)
NSERC, Discovery grant competition
$55,000

As Co-Investigator:

2019-2024 Using MRI imaging to develop a personalized risk-based breast cancer screening strategy.
Investigators: Martel A & Brooks J; Co-investigators: Astley S, **Briollais L**, Curpen B, Warner E.
CHIR project grant. $925,650

2017-2022 Building Knowledge and a foundation for HeALthy lIfe trajectories: BUKHALI Trial.
Investigators: Lye S, Matthews S, Norris S, Richter L (PIs), **Briollais** L et al.
$2,478,000
CIHR team grant: Healthy Life Trajectories Initiative (HeLTI) – South-Africa

2018-2019 Understanding early life origins of sex difference in insulin sensitivity
Luo ZC, **Briollais L**, Kingdom J, Lye S, Murphy K, Pausova Z.
$75,000.
CIHR Catalyst Grant: Sex as a Variable in Biomedical Research

2017-2020 Collaborating Centre for Statistical Omics
Investigators: Bull S (PI), **Briollais L** et al.
$50,000
CANSSI (Canadian Statistical Science Institute) Health Science

2017-2020 Novel germline mutation in the Kallikrein gene family and predisposition for aggressive prostate cancer.
Investigators: Zlotta A (PI), **Briollais L**, Fleshner N, Recker F, Kwiatkosvski M, Diamandis E.
Requested: $1,489,000.
Prostate Cancer Canada – Movember translation acceleration grant.

2016-2020 Lipid signatures of plasma-derived exosomes as markers of health and disease in pregnancy
Investigators: Caniggia I (PI), **Briollais L**, Post M, Bocking A
Requested: $1,305,000.
NIH – R01

GRANTS APPLIED FOR

2021-2025 CIHR project grant. Role of Breastfeeding on Epigenetic Mechanisms Underlying Early-Life Growth Trajectories.
Investigators: **Briollais L (PI)**, Lye S, Matthews S, McGowan P, O'Connor D.
Requested: **$1,600,000**

2021-2025 CIHR Team Grant: Canadian Microbiome Initiative. Programming the gut microbiome for child growth and development: a multi-national intervention study.
Investigators: **Comelli E (PI)**, Briollais L, O'Connor D, Connor K, Birken C, Lye S, Dennis CL, Matthews S, etc.

COMPLETED GRANTS (within past 5 years)

As PI or Co-PI:

2015-2018 Evaluation of Screening and Treatment Interventions Among Members of Breast Cancer BRCA1/2 Mutation Positive Families
Investigators: **Briollais L** (PI), Andrulis I, Knight J, Terry MB, Choi Y.
Canadian Breast Cancer Foundation
$449,139

2013-2016 Development, Application and Evaluation of Multistate Models for Risk Estimation and Screening Interventions in Lynch Syndrome Families and Familial Colorectal Cancer Type X Families
Investigators: **Briollais L** (PI), Kopciuk K, Choi YH, McLaughlin J, Cotterchio M, Gallinger S, Parfrey P
Canadian Institutes of Health Research, Operating grant
$273,334

2013-2016 Cancer risk factors and stability of telomere length during pregnancy; a pilot study to inform the use of telomere length as an intermediate outcome for cancer prevention studies
Investigators: Knight JA (PI), Anderson LN, **Briollais L**, Lye SJ
$25,000
Cancer Care Ontario Population Studies Research Network

2012-2015 Exploring the Complexity of Pediatric Brain Tumors with Advanced Genomics and Novel Statistical Methods
Investigators: **Briollais L** (PI), Hung R, McLaughlin J.
$75,000
McLaughlin Centre of University of Toronto

2007-2014 Gene-environment interactions underlying the developmental origins of health and disease.
Investigators: Lye S (PI), **Briollais L,** Pennell CE, Palmer LJ, et al.

$1,330,167
Canadian Institutes of Health Research

2012-2014 Early life gene-environment interactions and hypothalamic-pituitary-adrenal (HPA) axis function
Investigators: Anderson L (PI), **Briollais L** et al.
$51,666
Canadian Institutes of Health Research, Postdoctoral fellowship

INFRASTUCTURE FUNDING

2010-2015 A Clinical Phenotyping and Computational Facility for the Study of Complex Disease
Knight JA (PI), Bull SB, **Briollais L**, Logan A, Zinman B, Hung R, Lilge L
$1,209,767
Canadian Foundation for Innovation Leading Edge Fund, Ontario Research Fund

PUBLICATIONS

Supervised students and postdoctoral fellows are indicated with an asterisk.

Submitted

1. Sasaki A, Murphy KE, **Briollais L**, McGowan PO, and Matthews SG. Sex-specific DNA methylation profiles associated with maternal obesity in the blood of newborn term infants. Submitted to *FASEB*, June 2021.

2. **Briollais L**, Rustand D*, Wu Y*, Govinda Rajan S*, McGowan P, Matthews S, Lye S. Role of Breastfeeding on Epigenetic Mechanisms Underlying Early-Life Growth Trajectories. Submitted to *Genome Medicine*, June 2021.

3. Rustand D*, Rue H, Van Niekerk J, Tournigand C, Rondeau V, **Briollais L**. Bayesian Estimation of Two-Part Joint Models for a Longitudinal Semicontinuous Biomarker and a Terminal Event with R-INLA: Interests for Cancer Clinical Trial Evaluation. Submitted to *Statistics in Medicine*, June 2021.

4. Rustand D*, **Briollais L**, Rondeau V. A marginal two-part joint model for a longitudinal biomarker and a terminal event with application to advanced head and neck cancers. Submitted to *Stat Methods Med Res*., June 2021.

5. Wang N*, Massam H, **Briollais L**. The Birth-Death MCMC algorithm for mixed graphical model learning with application to genomic data integration. Submitted to *Annals of Applied Statistics*, May 2021.

Accepted

6. Choi YH, Terry MBT, MacInnis RJ, Hopper JL, Colonna S, Buys SS, Daly MB, Andrulis IL, Kurian AW, John EM, **Briollais L**. Risk-Reducing Salpingo Oophorectomy in Reducing Breast Cancer Risk in Women with BRCA1/2 mutations. Caution needed-Reply. *JAMA Oncology*, 2021; Online ahead of print.

7. Choi YH, Jung H*, Buys S, Daly M, John E, Hopper J, Andrulis I, Terry MB, **Briollais L**. A Competing Risks Model with Binary Time Varying Covariates for Estimation of Breast Cancer Risks in *BRCA1* Families. Accepted in *Stat Methods Med Res*., 2021; Online ahead of print.

8. Win AK, Dowty JG, Reece JC, Lee G, Templeton AS, Plazzer J-P, Buchanan DD, Akagi K, Aksoy S, Alonso A, Alvarez K, Amor DJ, Ankathil R, Aretz S, Arnold JL, Aronson M, Austin R, Backman A-S, Broeke SB, Barca-Tierno V, Barwell J, Bernstein I, Berthet P, Betz B, Bignon Y-J, Boisjoli T, Bonadona V, **Briollais L**, ..., Hopper JL, Haile RW, Macrae FA, Möslein G, Jenkins MA. Variation in the Risk of Colorectal Cancer for Lynch Syndrome. *Lancet Oncology* 2021; 22: 1014-22.

9. Choi YH, Terry MBT, MacInnis RJ, Hopper JL, Colonna S, Buys SS, Daly MB, Andrulis IL, Kurian AW, John EM, **Briollais L**. Risk-Reducing Salpingo Oophorectomy in Reducing Breast Cancer Risk in Women with BRCA1/2 mutations. *JAMA Oncology*, 2021; 7(4): 1014-1022.

10. Xu J*, Xu W, **Briollais L.** A Novel Bayesian Region-Based Analysis for Next Generation Sequencing Data. *Biometrics* 2021; 77(1): 316-328.

11. Abdul-Hussein A, Kareem A, Tewari S, Bergeron J, **Briollais L**, Challis JRG, Davidge ST, Delrieux C, Fortier I, Goldowitz D, Nepomnaschy P, Wazana A, Connor KL. Early life risk and resiliency factors and their influences on developmental outcomes and disease pathways: a rapid evidence review of systematic reviews and meta-analyses. J Dev Orig Health Dis. 2020 Aug 4:1-16.

12. Wu YY, Dennis CL, Lye S, **Briollais L**. Exclusive breastfeeding can attenuate body-mass-index increase among genetically susceptible children: a longitudinal study from the ALSPAC cohort. *PLoS Genetics 2020: 16(6):e1008790.*

13. Choi YH, **Briollais L**, He W, Kopciuk K. FamEvent: An *R* Package for Generating and Modeling Time-to-Event Data in Family Designs. *Journal of Statistical Software, In Press.*

14. Rustand D*, **Briollais L**, Tournigang C, Rondeau V. Two-part joint model for a longitudinal semicontinuous marker and a terminal event with application to metastatic colorectal cancer data. *Biostatistics 2020, In Press.*

15. Choi YH, Jacqmin-Gadda H, Król A*, Parfrey P, **Briollais L**, Rondeau V. Joint nested frailty models for clustered recurrent and terminal events: An application to colonoscopy screening visits and colorectal cancer risks in Lynch Syndrome families. Stat Methods Med Res. 2020, 29(5):1466-1479.

16. Dimitromanolakis A*, Xu J*, Krol A*, **Briollais L**. sim1000G: a user-friendly genetic variant simulator in R for unrelated individuals and family-based designs. BMC Bioinformatics. 2019 Jan 15;20(1):26.

17. Choi YC, Lakhal-Chaieb L, Krol A*, Yu B*, Buchanan D, Ahnen D, Le Marchand L, Newcomb PA, Win AK, Jenkins M, Lindor NM, **Briollais L**. Risks of colorectal cancer and cancer-related mortality in Familial Colorectal Cancer Type X and Lynch Syndrome families. J Natl Cancer Inst. 2019, 111(7):675:683.

18. **Briollais L**, Bristow R, Boutros P, the PRATICAL consortium, Zlotta A. Comment to Correspondence Re: Germline Mutations in the Kallikrein 6 region and Predisposition for Aggressive Prostate Cancer. Published online J Natl Cancer Inst. 2017, 109:12.

19. Zhang J, Shynlova O, Sabra S, Bang A, **Briollais L**, Lye SJ. Immunophenotyping and activation status of maternal peripheral blood leukocytes during pregnancy and labour, both term and preterm. J Cell Mol Med. 2017;21(10):2386-2402.

20. Wu YY*, Lye S, **Briollais L**. The Role of Early-Life Growth Development, *FTO* gene and Exclusive Breastfeeding on Child BMI trajectories. International Journal of Epidemiology 2017 46(5):1512-1522.

21. **L. Briollais**, H. Ozcelik, M. Kwiatkowski, J. Xu*, S. Savas, F. Recker, C. Kuk, S. Hanna, N. Fleshner, T. Juvet, M. Friedlander*, H. Li, K. Chadwick, J. Trachtenberg, A. Toi, T. van der Kwast, B. Bapat, E.P. Diamandis, P.C. Boutros, A.R. Zlotta. Fine-mapping of the *Kallikrein* Region supports a role for the *Kallikrein* 6 region in Genetic Predisposition for Aggressive Prostate Cancer: Results from a Canadian Cohort and the Swiss arm of the European Randomized Study for Prostate Cancer Screening. J Natl Cancer Inst. 2017 Apr 1;109(4). doi: 10.1093/jnci/djw258.

22. Choi YH, **Briollais** L, Win AK, Hopper J, Buchanan D, Jenkins M, Lakhal-Chaieb L. Modelling of Successive Cancer Risks in Lynch Syndrome Families in the presence of competing risks using Copulas. Biometrics 2017; 73(1): 271-282. doi: 10.1111/biom.12561.

23. Heng YJ, Pennell CE, McDonald SW, Vinturache AE, Xu J*, Lee M, **Briollais L**, Lyon AW, Slater DM, Bocking AD, Dolan SM, Tough SC, Lye SJ. Gene Expression in Maternal Whole Blood Predicts Spontaneous Preterm Birth in Asymptomatic Women as Early as 18 Weeks of Gestation. *PLoS One*, 2016; 11(6): e0155191.

24. P.G. Parmar*, H.R. Taal, N.J. Timpson, E. Thiering T. Lehtimäki, M Marinelli, P.A. Lind, G. Verwoert, V. Aalto, A.G. Uitterlinden, **L. Briollais**, et al. International GWAS Consortium Identifies Novel Genes Associated with Blood Pressure in Children and Adolescents. *Circulation: Cardiovascular Genetics* 2016; 9: 266-78.

25. **Briollais L**, Dobra A, Liu J*, Friedlander M*, Ozcelik H, Massam H. A Bayesian graphical model for genome-wide association studies (GWAS). Annals of Applied Statistics 2016; 10(2): 786-811.

26. White SW, Marsh JA, Lye SJ, **Briollais L**, Newnham JP, Pennell CE. Improving customized fetal biometry by longitudinal modelling. J Matern Fetal Neonatal Med. 2015; 4:1-7.

27. Wu YY*, Wong A, Monette G and **Briollais L**. Evaluation of Third-order Method for the Test of Variance Component in Linear Mixed Models. Open Journal of Statistics 2015; 5: 233-244.

28. NM Warrington*, LD Howe, L Paternoster, M Kaakinen, S Herrala, V Huikari, Y Wu, JP Kemp, NJ Timpson, B St. Pourcain, G Davey-Smith, M-R Jarvelin, CE Pennell, DM Evans, DA Lawlor, **L Briollais**, LJ Palmer. A Genome-Wide Association Study of Body-Mass-Index across Early Life. Int J Epidemiol. 2015; 44(2): 700-12.

29. Grant RC, Selander I, Connor AA, Selvarajah S, Borgida A, **Briollais L**, Petersen GM, Lerner-Ellis J, Holter S, Gallinger S. Prevalence of germline mutations in cancer predisposition genes in patients with pancreatic cancer. Gastroenterology 2015; 148(3):556-64.

30. Louise S*, **Briollais L**, Mori TA, Mattes E, McCaskie PA, Pennell CE, Palmer LJ and Beilin LJ. Monoamine oxidase a gene polymorphisms common to blood pressure and depression scores in Caucasian children. *J Genet Stud*. 2014; 2:2.

31. Kang S*, Savas S, Liu J*, Ozcelik H, **Briollais L**. Inferring Gene Network from Candidate SNP Association Studies using Bayesian Graphical Model: Application to a Breast Cancer Case-Control Study from Ontario. Human Heredity, 2014; 78(3):140-152.

32. Warrington NM*, Tilling K, Howe L, Paternoster L, Pennell CE, Wu YY*, **Briollais L**. Robustness of the linear mixed effects model to distribution assumptions and consequences for genome-wide association studies. Statistical Applications in Genetics and Molecular Biology 2014; 13(5):567-87.

33. Anderson LN, **Briollais** L, Atkinson HC, Marsh JA, Xu J, Connor KL, Matthews SG, Pennell CE, Lye SJ. Investigation of genetic variants, birthweight and hypothalamic-pituitary-adrenal (HPA) axis function suggests a genetic variant in the SERPINA6 gene is associated with corticosteroid binding globulin among adolescents in the Western Australia Pregnancy Cohort (Raine) Study. PLoS One. 2014; 9(4):e92957.

34. **Briollais L**, Durrieu G. Application of Quantile Regression to Recent Genetic and -omic Studies. Human Genetics 2014; 133(8): 951-66.

35. Wu YY*, **Briollais L**. Association of a Body Mass Index Genetic Risk Score with Growth throughout Childhood and Adolescence. BMC proceedings 2014; 8 (Suppl 1): S92.

36. Abarin T*, Li H, Wang L, **Briollais L** (2014) On Method of Moments Estimation in Linear Mixed Effects Models with Measurement Error on Covariates and Response with Application to Longitudinal studies of Gene-Environment Interaction. Statistics in Biosciences 6:1-18. doi:10.1007/s12561-012-9074-5.

37. Howe LD, Parmar PG*, Paternoster L, Warrington NM, Kemp JP, **Briollais L**, Newnham JP, Timpson NJ, Smith GD, Ring SM, Evans DM, Tilling K, Pennell CE, Beilin LJ, Palmer LJ, Lawlor DA. Genetic influences on trajectories of systolic blood pressure across childhood and adolescence. Circ Cardiovasc Genet 2013; 6(6): 608-14.

38. Warrington NM*, Howe L, Wu YY*, Timpson NJ, Tilling K, Pennell CE, Newnham J, Davey-Smith G, Palmer LJ, Beilin LJ, Lye S, Lawlor DA, **Briollais L**. Association of a Body Mass Index Genetic Risk Score with Growth throughout Childhood and Adolescence. PLoS ONE 2013; 8(11): e79547**.**

39. Choi YH*, **Briollais L**, Parfrey P, Green J, Kopciuk K. Estimating successive cancer risk in Lynch Syndrome families using a progressive three-state model. Statistics in Medicine, 2013; 33: 618-38. doi: 10.1002/sim.5938.

40. Kron K, Trudel D, Pethe VV, **Briollais L**, Fleshner NE, van der Kwast TH, Bapat B. Altered DNA methylation landscapes of polycomb-repressed loci are associated with Gleason score and ERG oncogene expression in prostate cancer. Clin Cancer Res. 2013; 19(13): 3450-61.

41. Agim S, Esendal M, **Briollais L**, Uyan O, Meschian M, Mendoza Martinez LA, Ding Y, Basak N, Ozcelik H. (2013) Discovery, validation and characterization of ERBB4 and NGR1 haplotypes using data from three genome-wide association studies of schizophrenia. PLoS One 8(1):e53042.

42. Warrington NM*, Wu YY*, Pennell CE, Marsh JA, Beilin LJ, Palmer LJ, Lye SJ, **Briollais L**. (2013) Modelling BMI trajectories in children for genetic association studies. PloS One 8(1):e53897

43. Abarin T*, Wu YY*, Warrington N*, Lye S, Pennell C, **Briollais L**. (2013) The impact of breastfeeding on FTO-related BMI growth trajectories. International Journal of Epidemiology 41(6):1650-60.

44. Olkhov-Mitsel E, Van der Kwast T, Kron KJ, Ozcelik H, **Briollais L**, Massaey C, Recker F, Kwiatkowski M, Fleshner NE, Diamandis EP, Zlotta AR, Bapat B (2012) Quantitative DNA methylation analysis of genes coding for Kallikrein-related peptidases 6 and 10 as biomarkers for prostate cancer. Epigenetics 1;7(9).

45. Parmar PG*, Marsh JA, Taal HR, Kowgier M, Uitterlinden AG, Rivadeneira F, **Briollais L**, Newnham JP, Hofman A, Lye SJ, Steegers EAP, van Duijn CM, Palmer LJ, Jaddoe VWV, Pennell CE (2012) Polymorphisms in Genes within the IGF-axis Influence Antenatal and Postnatal Growth. Journal of Developmental Origins of Health and Disease. 2: S141-S.

46. Marsh JA, Pennell CE, Warrington NM*, Mook-Kanamori D, **Briollais L**, Lye SJ, Beilin LJ, Steegers E, Hofman A, Jaddoe VWV, Newnham JP and Palmer LJ (2012). Fat mass and obesity-associated obesity-risk genotype is associated with lower foetal growth: an effect that is reversed in the offspring of smoking mother. Journal of Developmental Origins of Health and Disease 3:10-20.

47. Louise S*, Warrington NM*, McCaskie PA, Oddy WH, Zubrick SR, Hands B, Mori TA, **Briollais L**, Silburn S, Palmer LJ, Mattes E, Beilin LJ (2012) Associations between anxious-depressed symptoms and cardiovascular risk factors in a longitudinal childhood study. Prev Med 54(5): 345-50.

48. Fehringer G, Liu G, **Briollais L**, Brennan P, Amos C, Spitz M, BickebŽller H, Wichmann HE, Risch A, Hung R (2012) Comparison of pathway analysis approaches using lung cancer GWAS data sets. PLoS One, 7(2):e31816.

49. Islam M, Chowdhury R*, **Briollais L**. (2012) A bivariate binary model for testing dependence in outcomes. Bulletin of the Malaysian Mathematical Society series 2, 35(4):845-858.

50. Tram E, Ibrahim-Zada I, **Briollais L**, Knight JA, Andrulis IL, Ozcelik H (2011) Identification of germline alterations of the mad homology 2 domain of SMAD3 and SMAD4 from the Ontario site of the breast cancer family registry (CFR). Breast Cancer Res. 11; 13(4):R77.

51. Savas S, Azorsa DO, Jarjanazi H, Ibrahim-Zada I, Gonzales IM, Arora S, Henderson MC, Choi YH, **Briollais L**, Ozcelik H, Tuzmen S (2011) NCI60 cancer cell line panel data and RNAi analysis help identify EAF2 as a modulator of simvastatin and lovastatin response in HCT-116 cells. PLoS One 6(4):e18306.

52. Sovio U, Mook-Kanamori DO, Warrington NM*, Lawrence R, **Briollais L**, Palmer CN, Cecil J, Sandling JK, SyvŁnen AC, Kaakinen M, Beilin LJ, Millwood IY, Bennett AJ, Laitinen J, Pouta A, Molitor J, Davey Smith G, Ben-Shlomo Y, Jaddoe VW, Palmer LJ, Pennell CE, Cole TJ, McCarthy MI, JŁrvelin MR, Timpson NJ; Early Growth Genetics Consortium (2011) Association between common variation at FTO locus and changes in body mass index from birth to adolescence: Longitudinal analysis of over 19,000 children of European ancestry. PLOS Genetics 7(2):e1001307.

53. Liu L, Kron KJ, Pethe VV, Demetrashvili N*, Nesbitt ME, Trachtenberg J, Ozcelik H, Fleshner NE, **Briollais L**, van der Kwast TH, Bapat B (2011) Association of tissue promoter methylation levels of APC, TGFb2, HOXD3, and RASSF1A with prostate cancer progression. Int J Cancer 129(10): 2454-62.

54. Sow M*, Durrieu G, **Briollais L**, Ciret P, Massabuau JC (2011) Modeling high-frequency serial valvometry data: a kernel-regression approach. Environmental Monitoring and Assessment 182(1-4):155-70.

55. Choi YH*, **Briollais L** (2011) An EM Composite likelihood for multistage sampling of family data. Statistica Sinica 21: 231-253.

56. Hasan T*, Choi Y*, **Briollais L** (2011) A Sequential Approach for Clustered Survival Data in Family Studies Based on a Weighted Log-Rank Statistic. Journal of Applied Statistical Science 18: 1-16.

57. Savas S, **Briollais L**, Ibrahim-Zada I, Jarjanazi H, Choi YH*, Musquera M, Fleshner N, Venkateswaran V, Ozcelik H (2010) A Whole-Genome SNP Association Study of NCI60 Cell Line Panel Indicates a Role of Ca Signaling in Selenium Resistance. Plos One Sept 7, 5(7).

58. Kron KJ, Liu L, Pethe VV, Demetrashvili N*, Nesbitt ME, Trachtenberg J, Ozcelik H, Fleshner NE, **Briollais L**, van der Kwast TH, Bapat B (2010) DNA methylation of HOXD3 as a marker of prostate cancer progression. Laboratory Investigation 90(7):1060-7.

59. Demetrashvili N*, Kron K, Pethe V, Bapat B and **Briollais L** (2010). How to Deal with Batch Effect in Sequential Microarray Experiments? Molecular Informatics 29(5):387-393.

60. Planque C, Choi YH*, Guyetant S, Heuzé-Vourc'h N, **Briollais L**, Courty Y (2010) Alternative splicing variant of kallikrein-related peptidase 8 as an independent predicator of unfavorable prognosis in lung cancer. Clinical chemistry 56(6):987-97.

61. Kopciuk KA, Choi YH*, Parkhomenko E*, Parfrey P, McLaughlin J, Green J, **Briollais L**. (2009) Penetrance of HNPCC-related cancers in a retrolective cohort of 12 large Newfoundland families carrying a MSH2 founder mutation: an evaluation using modified segregation models. Hered Cancer Clin Pract 7(1):16.

62. Choi YH*, Cotterchio M, McKeown-Eyssen G, Neerav M, Bapat B, Boyd K, Gallinger S, McLaughlin J, Aronson M, **Briollais L** (2009) Penetrance of colorectal cancer among MLH1/MSH2 carriers participating in the colorectal cancer familial registry in Ontario. Hered Cancer Clin Pract. 23;7(1):14.

63. Wu LY, Chipman HA, Bull SB, **Briollais L**, Wang K. (2009) A Bayesian segmentation approach to ascertain copy number variations at population level. Bioinformatics 25(13):1669-79.

64. Heuzé-Vourc´h N, Planque C, Guyetant S, Coco C, Brillet B, Blechet C, Parent C, **Briollais L**, Reverdiau P, Jourdan M-L and Courty Y (2009) High Kallikrein-Related Peptidase 6 in Non-Small Cell Lung Cancer Cell: a Proliferative and a Poor Prognosis Factor. J Cell Mol Med May 1.

65. Kron K, Pethe V, **Briollais L**, Sadikovic B, Ozcelik H, Sunderji A, Venkateswaran V, Pinthus J, Fleshner N, van der Kwast T, Bapat B (2009) Discovery of novel hypermethylated genes in prostate cancer using genomic CpG island microarrays. PLoS ONE 4 (3).

66. Durrieu G, **Briollais L** (2009). Sequential designs for microarray experiments. Journal of the American Statistical Association 104:650-660.

67. Choi YH*, Kopciuk K, **Briollais L** (2008) Bias and efficiency in family-based designs for estimating the risk associated with mutated genes involved in complex diseases. Hum Hered. 66:238-251.

68. Ghosh S, Babron MC, Amos CI, **Briollais L**, Chen P, Chen WV, Chiu WF, Drigalenko E, Etzel CJ, Hamshere ML, Holmans PA, Margaritte-Jeannin P, Lebrec JJ, Lin S, Lin WY, Mandhyan DD, Nishchenko I, Schaid DJ, Seguardo R, Shete S, Taylor K, Tayo BO, Wan S, Wei LY, Wu CO, Yang XR (2007) Linkage analyses of rheumatoid arthritis and related quantitative phenotypes: the GAW15 experience. Genet Epidemiol 31 Suppl 1:S86-95.

69. Briollais L, Durrieu G, Upathilake R (2007) Novel Approach for Genome Scan Meta-Analysis of Rheumatoid Arthritis: A Kernel-Based Estimation Procedure. BMC Proceedings Suppl.1: S96.

70. Onay V, Aaltonen K, **Briollais** L, Knight JA, Pabalan N, Kilpivaara O, Andrulis IL, Blomqvist C, Nevanlinna H, Ozcelik H (2008) Combined effect of CCDN1 and COMT polymorphisms and increased breast cancer risk. BMC Cancer 14;8:6.

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90. Valeri A, Berthon P, Fournier G, Buzzi JC, **Briollais L**, Meria P, Blanche H, Bellanne-Chantelot C, Teillac P, Demenais F, Mangin P, Cohen N, Le Duc A, Cussenot O (1996) Etude PROGENE, projet français d'analyse génétique du cancer de la prostate familial: recrutement et analyse. Progrès en Urologie 6, 226-35 (In French).

91. Valeri A, Berthon P, Fournier G, Meria P, **Briollais L** et al. (1995). Etude génétique du cancer de la prostate familial. Prostate Tumeurs 18, 10-4 (In French).

BOOK CHAPTERS

1. Dobra, A., **Briollais, L**., Jarnazi H, Ozcelik H, Massam H. Applications of the mode oriented stochastic search (MOSS) algorithm for discrete multi-way data to genomewide studies. In Bayesian Modeling in Bioinformatics Taylor & Francis, D. Dey, S. Ghosh and B. Mallick (eds.), 2011, pages 63-94.

2. **Briollais L** and Durrieu G. Quantile regression for genetic and genomic applications. In Handbook of quantile regression. Chapman and Hall/CRC Handbooks of Modern Statistical Methods. Koenker, Chernozhukov, He and Peng (eds.). October 25, 2017.

PROCEEDINGS

1. Choi YH, **Briollais L**. Impact of competing risks on the risk estimation of multiple cancers in family studies. In Joint Statistical Meeting Proceedings, Alexandria, VA: American Statistical Association. Boston, Aug 2-7, 2014.
2. **Briollais L**, Dobra A, Massam H. Detection of gene by gene and gene by environment interactions in genome-wide association studies (GWAS) through Bayesian graphical models. Proceeding of the Société Française de Statistique, 6p. Rennes, June 2-6, 2014.
3. **Briollais L**, Choi YH. An EM Composite Likelihood Approach based on Frailty Model for Family Studies of Unknown Genetic Factors with Incomplete Genetic Data. Proceeding of the Société Française de Statistique, 6p.Toulouse, May 27-31, 2013.
4. **Briollais L**, Choi YH, Yildaz Y. Multistate models for the evaluation of screening interventions in family designs. In Joint Statistical Meeting Proceedings, Alexandria, VA: American Statistical Association. Montreal, Aug 3-8, 2013.
5. Choi Y-H, **Briollais L**. A frailty-model-based approach to estimating the age-dependent penetrance function of a gene mutation using family-based study designs. In Joint Statistical Meeting Proceedings, Alexandria, VA: American Statistical Association. Vancouver, Jul 31-Aug 5, 2010.
6. M Sow, G Durrieu, **L Briollais**. A robust statistical framework for eQTL analysis. In Joint Statistical Meeting Proceedings, Alexandria, VA: American Statistical Association. Vancouver, Jul 31-Aug 5, 2010.
7. Liu J, **Briollais L**, Dobra A, Massam H. Impact of informative prior in discrete Bayesian graphical models: application to genome-wide association studies. In Joint Statistical Meeting Proceedings, Alexandria, VA: American Statistical Association. Washington D.C., Aug 1-8, 2009.

SOFTWARES

1. *R* package **GenMOSS** implementing Bayesian graphical models for GWAS analysis.
2. *R* package **GenMOSSplus** implementing Bayesian graphical models for GWAS analysis and various preprocessing steps for GWAS.
3. *R* package **FamEvent** to generate family data for diseases with variable age at onset.
4. *R* package **RareBF** for analyzing rare variants from sequencing studies using a Bayes factor approach.
5. *R package* **Sim1000G** *for simulating sequencing data according to the 1000 genomes.*

PRESENTATIONS

(I=International; N=National; L=Local)
Note: Only my own presentations are included here. Students' and collaborators' presentations where I was involved are not given.

Invited

- Polygenic prediction via Bayesian regression and continuous shrinkage priors. Statistical Genetic seminar, April 2020, Toronto. ***(L)***
- The Role of Early-Life Growth Development, Genetic Factors and Exclusive Breastfeeding on Child BMI trajectories. Epidemiology and Biostatistics Seminar, Western University. March 2019. ***(L)***
- Breastfeeding modulates growth trajectory in children. Cuba-Canada Maternal-Child Health Symposium. March 2019. ***(I)***
- New Statistical Methods for Family-Based Sequencing Studies workshop (18w5154) – Banff international Workshop – Aug 2018 ***(I)***
- Mount Sinai Hospital/University Health Network Genetic Medicine Grand Rounds. May 2018. Role of Breastfeeding on Epigenetic Mechanisms Underlying Early-Life Growth Trajectories. ***(L)***
- Levin Lecture Series in Biostatistics – Columbia University, New-York. May 4, 2017. ***(I)***
- A novel region-based Bayesian approach for genetic association with next generation sequencing data. Biostatistics Training Initiative, OICR, April 25, 2017.
- The *KLK6* study. PRACTICAL-ELLIPSE annual meeting. 27-28 March 2017, London, UK. ***(I)***
- Replicability analysis for genome-wide association studies. Statistical Genetic seminar, 12 May 2017, Toronto. ***(L)***
- Modelling BMI growth trajectories and impact on intervention programs. Target Kids science meeting at Sick Kids hospital. Feb 6th, 2016, Toronto. ***(L)***
- Implementing and evaluating genetic risk-stratified screening strategies for common cancers. Statistical Genetic seminar, April 28th, 2016, Toronto. ***(L)***
- A novel region-based Bayesian approach for genetic association with next generation sequencing (NGS) data. BIT seminar series, Toronto, April 25, 2017. ***(L)***
- Quantile regression for genetic and genomic applications. International workshop on quantile regressions. Cambridge, December 2015. ***(I)***
- Bayesian graphical models for gene network analysis in large-scale problems. Canadian Statistical Association Annual Meeting, Halifax, Canada, June 2015 ***(N)***
- Evaluation of screening efficiency with colonoscopy in Lynch Syndrome families. Colon CFR. Complex disease epidemiology discussion group. Toronto, Canada, April 2015. ***(L)***
- Modeling health trajectories and impact on prevention programs. Big Data for Health Workshop. Toronto, July 2014. ***(L)***
- Detection of gene by gene and gene by environment interactions in Genome-wide association studies (GWAS) through Bayesian graphical models. Banff International workshop, July 2014. ***(I)***
- Statistical challenges in modeling time-to-event data in family studies. Lessons learned from the analysis of Lynch syndrome and breast cancer families. Statistical Society of Canada annual meeting, Toronto, May 25, 2014. ***(N)***
- Modeling health trajectories and impact on prevention programs. LTRI annual retreat. Orillia, Canada, May 2014. ***(L)***
- Detection of SNP by SNP interactions in Genome-wide association studies (GWAS) through Bayesian graphical models. Journée de Statistiques, Société Française de Statistiques, Rennes, France, June 2014. ***(I)***
- Predicting prostate cancer progression through gene network analysis of methylation data. Second Annual Canadian Human and Statistical Genetic meeting, Esterel, Quebec, April 2013. ***(N)***
- Detection of SNP by SNP interactions in Genome-wide association studies (GWAS) through Bayesian graphical models. Dept. of Mathematics & Statistics, Laval University, Oct 2013. ***(N)***
- Graphical Models in Genetic Association Studies. Dept. of Mathematics & Statistics, University of South Brittany, France (December 2013) ***(I)***
- An EM Composite likelihood approach for family studies with incomplete genetic data. Workshop on Composite Likelihood Methods, Banff, Canada, 22-27 April 2012. ***(I)***
- A Bayesian Graphical Model for Genome-wide Association Studies (GWAS). Biostatistics Dept., McGill University. September 2011. ***(N)***
- A General Statistical Framework for Genome-wide Association Studies (GWAS) Based on Bayesian Graphical Modeling. Statistics Dept., York University, Toronto, July 2011. ***(L)***

Contributed

- A Novel Region-Based Bayesian Approach for Genetic Association with Next Generation Sequencing (NGS) Data. XXIXTH INTERNATIONAL BIOMETRIC CONFERENCE. Barcelona, Spain, 8-13 July 2018. ***(I)***
- Role of Breastfeeding on Epigenetic Mechanisms Underlying Early-Life Growth Development and the Development Origin of Obesity. DOHAD bi-annual meeting. Rotterdam 15-18 Oct. 2017. ***(I)***
- A Novel Bayesian Approach for Region-Based Analysis of Next Generation Sequencing Data. ProbGen17 Probabilistic Modeling in Genomics, 18-20 Sept 2017, Aarhus, Denmark. ***(I)***
- Modelling successive time-to-event outcomes in presence of competing risk events using Copulas. French Statistical Association annual meeting, Avignon, France, May 29th to June 2nd, 2017. ***(I)***
- Markov-Renewal Multistate Model for Colorectal Cancer Screening Evaluation in Lynch Syndrome families. International Biometric Conference, Victoria, Canada, July 10-15th, 2016. ***(I)***
- The *R* package genMOSS for Genome-wide Association Studies (GWAS). The American Society for Human Genetics, Vancouver, Canada, Oct 18-22th, 2016. ***(I)***
- Evaluation of screening efficiency with colonoscopy and risk estimation of second cancers in Lynch Syndrome families. Colon CFR Steering Committee. Honolulu, Hawaii, June 23-25, 2015. ***(I)***
- Evaluation of screening efficiency with colonoscopy in Lynch Syndrome families. Colon CFR Steering Committee. Kauai, Hawaii, 4-5 Sept 2014. ***(I)***
- An EM composite likelihood approach based on frailty model for family studies of unknown genetic factors with incomplete genetic data. French Statistical Society Annual Meeting, Toulouse, France, May 27-31 2013. ***(I)***
- Multistate models for the evaluation of screening interventions in family designs. Joint Statistical Meeting, Montreal, Canada, August 3-8, 2013. ***(I)***
- Composite likelihood estimation in family studies with incomplete genetic data. International Symposium in Statistics (ISS) on Longitudinal Data Analysis Subject to Outliers, Measurement Errors, and/or Missing Values. St. John's, Canada, July 16-18, 2012. ***(N)***
- A General Statistical Framework for Genome-wide Association Studies (GWAS) Based on Bayesian Graphical Modeling. International Biometric Society, Bordeaux, France, April 2011. ***(N)***
- Bayesian Graphical Models (BGMs) for Genetic Association Studies. Annual meeting of the Statistical Society of Canada (SSC), Acadia University, Wolfville, Canada, June 2011. ***(I)***

Contributions to the University (Dalla Lana School of Public Health – University of Toronto)

- Student supervision (MSc, PhD)
- Participate to admission committees (MSc, PhD) (yearly)
- Participate to thesis committees (MSc, PhD)
- Teaching Activities
- Seminars and lectures given regularly
- Member of PhD students' progress evaluation committee
- Member of MPH in Data Science Steering Committee
- Member of the Biostatistics Curriculum Committee
- Evaluation of promotion applications within the Biostatistics division
- Mentor in Statistical Genetics, CIHR Strategic Training for Advanced Genetic Epidemiology (STAGE)
- Evaluation of CIHR Strategic Training for Advanced Genetic Epidemiology (STAGE) PhD and postdoc applications

Teaching (Dalla Lana School of Public Health – University of Toronto)

- CHL8001H F2: Introduction to Joint Modelling in Health Research. Main Instructor, summer 2019 and 2020. MSc and PhD level, enrolment of 16 students (including 13 registered) in 2020 and 7 students (2 registered) in 2019. Time commitment per year: 18 hours teaching + 120 hours for lecture/assignment preparation and students' grading.
- CHL5210: Categorical Data Analysis. Co-instructor in 2011, 2012, 2013 and 2 lectures given in 2018. MSc and PhD level, enrolment about 25 students. Time commitment per year: 8 hours teaching + 120 hours for lecture/assignment preparation and students' grading.
- CHL7001H: Introduction to the Likelihood paradigm. Co-instructor in 2014. MSc and PhD level, enrolment about 8 students. Time commitment per year: 8 hours teaching + 120 hours for lecture/assignment preparation and students' grading.
- CHL5224H: Statistical Genetics. Co-instructor in 2015. MSc and PhD level, enrolment about 25 students. Time commitment per year: 8 hours teaching + 120 hours for lecture/assignment preparation and students' grading.

- CHL7001: Statistical Models on Complex Human Genetic Diseases. Lectures given in 2012 and 2013. MSc and PhD level, enrolment about 8 students. Time commitment per lecture: 20 hours.
- CHL5228H: Statistical Methods for Genetics and Genomics - Research seminar and Journal club. One lecture given every year. MSc and PhD level, enrolment about 8 students. Time commitment per lecture: 20 hours.
- CHL5250H: Special topics in biostatistics. Help preparing a 6h tutorial on joint modelling taught by previous postdoc Agnieszka Krol in 2017. MSc and PhD level, enrolment about 25 students. Time commitment: 8 hours.

Student Supervision Activities

Actual Students

- Jingxiong Xu (2021-). Postdoctoral fellow. Bayesian analysis of next generation sequencing data.
- Konstantin Shestopaloff (2019-). Postdoctoral fellow. Modelling of polygenic risk score in longitudinal studies.
- Nanwei Wang (2017-). Postdoctoral fellow. Bayesian regression models for high-dimensional genetic data.
- Aisha Hammah (2020-). Co-supervisor. Master of Liberal Arts, Biology. (Harvard University).

Past Students

Postdoc fellows

- Fode Tounkara (2017-2019). Postdoctoral fellow. Modeling of successive and competing cancer events in Hereditary Breast Ovarian Cancer (HBOC) families.
- Changchang Xu (2018). Practicum student, PhD. Dalla Lana School of Public Health (Biostatistics), University of Toronto.
- Agnieszka Krol (2016-2017). Survival analysis models for Next Generation Sequencing (NGS) studies.
- Narges Nazeri Rad (2014-2016). Currently Project Manager at Cancer Care Ontario.
- Yan Yan Wu (2011-2014). Currently Assistant Professor in the Department of Public Health Studies, University of Hawaii, USA.
- Taraneh Abarin (2009-2011). Currently Assistant Professor in the Department of Mathematics and Statistics at Memorial University, NL, Canada
- Jinnan Liu (2007-2009). Currently statistician in a private company (USA).
- Sohee Kang (2006-2008). Currently Assistant Professor in the Department of Statistics, University of Toronto Scarborough, ON, Canada.
- Yun-Hee Choi (2005-2008). Currently Associate Professor in the Department of Epidemiology and Biostatistics, Western Ontario, ON, Canada.
- Tariq Hasan (2005-2006). Currently Associate Professor in the Department of Mathematics and Statistics, University of New Brunswick, NB, Canada
- Wenqinq He (2004). Currently Associate Professor in the Department of Statistical and Actuarial Science, Western University, ON, Canada
- Marcia Wang (2003-2005). Currently statistician in a pharmaceutical company (USA).

PhD students

- Denis Rustand (2017-2020). PhD student in Bordeaux, France. Joint models for the evaluation of cancer immune-therapies. (Co-supervision with Dr. Viriginie Rondeau, ISPED, University Bordeaux II).
- Jingxiong Xu (2013-2019). A Novel Bayesian Region-Based Analysis for Next Generation Sequencing Data. Defended Aug. 2019.
- Nicole Warrington (2011-2014). University of Western Australia (Co-supervisor). Currently postdoctoral student at the University of Queensland Diamantina Institute.
- Priya Parmar (2012-2015). University of Western Australia (Co-supervisor). Currently lecturer at Auckland University of Technology.
- Mohamedou Sow (2007-2011). University Bordeaux 1 (Co-supervisor). Currently research associate at CNRS, Bordeaux, France.

MSc and undergraduate students

- Boim Chang (2019-2020). MSc student (U. of T, Biostatistics). Application of joint modeling for cancer clinical trials.
- Arthur Fetiveau (2020). MSc student. University of South Britany (France). Statistical modelling of lipidomics data.
- Samyukta Govinda Rajan (2016-2017): Modeling of BMI trajectories in the ALSPAC cohort.
- Nina Zhang (2019-2020). Practicum student (U. of T, Biostatistics). Application of joint modelling to assess colorectal cancer risks in Lynch Syndrome families.
- Hae Young Jung (2017). MSc summer student. Modeling of successive and competing cancer events in Hereditary Breast Ovarian Cancer (HBOC) families.
- Samyukta Govinda Rajan (2016-2017): Modeling of BMI trajectories in the ALSPAC cohort.
- Jingchun Pei (2015-2016). MSc practicum, Application of multistate models for PSA screening evaluation
- Yuan Sun (2015). Undergraduate student, University of Toronto (Statistics). Supervised research project.
- Rosita Bajari (2014). MSc student, Ryerson University (Computer Science). Supervised research project.
- Ely Fish (2013). Undergraduate student, University of Toronto. Supervised research project.
- Razvan Romanescu (2012) MSc student, University of Toronto (Statistics). Supervised research project.
- Vanessa Lestang (2011) MSc student, University Bordeaux 2 (ISPED). Supervised Master I project.
- Mathieu Raimbault (2010). MSc student, University Bordeaux 2 (ISPED). Supervised Master I project.
- Nino Demetrashvili (2008-2009). MSc student, University of Toronto (Biostatistics). Supervised research project.
- Aditya Sagar (2008). Undergraduate student, Indian Institute of Technology. Supervised research project.
- Elena Parkhomenko (2004). MSc student, University of Toronto (Biostatistics). Supervised lab course.
- Yana Tcharaktchiev (2003). Undergraduate student, University of Waterloo (Computer Science). Supervised research project.

STUDENTS' COMMITTEES/THESIS EXAMINER

- MSc thesis committee member. Yuan Bian (2020). Dalla Lana School of Public Health (Biostatistics), University of Toronto. Supervisor: Shelley Bull.
- MSc thesis committee member. Kayla Abrego de Castillo (2019-2020). Department of Physiology, University of Toronto. Supervisor: Steve Lye.
- MSc thesis committee member. Susan Wamithi (2019-). Department of Physiology, University of Toronto. Supervisor: Steve Lye.
- MSc thesis committee member. Michela Panarella (2019). Dalla Lana School of Public Health (Biostatistics), University of Toronto. Supervisor: Shelley Bull.
- PhD thesis internal reviewer. Osvaldo Espin-Garcia (2019). Dalla Lana School of Public Health (Biostatistics), University of Toronto. Supervisor: Shelley Bull.
- External examiner of PhD defense. Amadou Diogo Barry (March 2019). UQAM, Dept. of Mathematics and Statistics.
- PhD thesis committee member. Sangook Kim (2018-). Dalla Lana School of Public Health (Biostatistics), University of Toronto. Supervisor: Lisa Strug.
- CIHR STAGE mentor and PhD thesis committee member. Matthew Warkentin (2018-). Dalla Lana School of Public Health (Epidemiology), University of Toronto. Supervisor: Rayjean Hung.
- External examiner of MSc defense. Daniel Prawira (Oct. 2017). Western University. Dept. of Epidemiology and Biostatistics.
- External examiner of PhD defense. Charlie Keown-stoneman (May 2017). Guelph University, Dept. of Mathematics and Statistics.
- Examiner for Departmental Oral Defense. David Soave, PhD student (Aug. 2016). Dalla School of Public Health (Biostatistcs), University of Toronto.
- External examiner of PhD defense. Martin Leclerc (Feb. 2016). Laval University, Dept. of Mathematics and Statistics.
- Examination Committee of PhD defense. Jessica Dennis (Jan 2016). Dalla School of Public Health (Epidemiology), University of Toronto.
- External examiner of PhD defense. Haiyan Yang (Feb 2014). Memorial University, Dept. of Mathematics and Statistics
- External examiner of PhD defense. Aung Ko Win (March 2014). University of Melbourne, School of Population and Global Health.
- External examiner of PhD defense. Matthew Kowgier (Oct 2011). Dalla School of Public Health

(Biostatistics), University of Toronto.